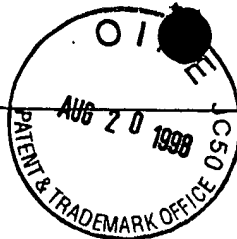


SEQUENCE LISTING



<110> Hayward, Nicholas K.
Weber, Gunther
Grimmond, Sean
Nordenskjold, Magnus
Larsson, Catharina

<120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
SAME

<130> DAVIES

<140> 08/765,588

<141> 1996-02-22

<160> 23

<170> PatentIn Ver. 2.0

<210> 1

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<222> (17)..(589)

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1

5

10

gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100

Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro

15

20

25

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148

Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met

30

35

40

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196

Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp

45

50

55

60

atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244

Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser

65

70

75

tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg 292
 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
 80 85 90

gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg 340
 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
 95 100 105

atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag 388
 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
 110 115 120

cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa 436
 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
 125 130 135 140

aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa 484
 Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
 145 150 155

gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc 532
 Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
 160 165 170

aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag 580
 Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
 175 180 185

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 Pro Arg Arg
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gaaccagatc tctcaccagg 649

<210> 2

<211> 191

<212> PRT

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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 180 185 190

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<220>

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 1 5 10 15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His

agactcagca ggggtgacttg cctcagaggc tatatcccag tgggggaaca aaggggagcc 743
 tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803
 ggctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863
 agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923
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 cctccccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tgggtacaaga 1043
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 <213> Nucleotide Sequence of SOM175

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 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
 130 135 140

a3
 cmf

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
145 150 155 160

Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
165 170 175

His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
180 185 190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
195 200 205

<210> 5

<211> 993

<212> DNA

<213> Nuc. Seq. of SOM175 Absent Exon 6

<220>

<221> CDS

<222> (3)..(566)

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1 5 10 15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
20 25 30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
35 40 45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
50 55 60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
65 70 75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
80 85 90 95

caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335

Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
100 105 110

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
115 120 125

aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431
Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro
130 135 140

cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc 479
Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys
145 150 155

cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag 527
Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
160 165 170 175

ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg 576
Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
180 185

cttttcagac tcagcagggg gacttgccctc agaggctata tcccagtgagg ggaacaaagg 636

ggagcctggg aaaaaacagc caagcccccagacctcagc ccaggcagaa gctgctctag 696

gacctggggc tctcagaggg ctcttctgcc atcccttgctc tccctgaggc catcatcaaa 756

caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata ccagctcagg 816

ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat cttacaactg 876

gctcttctc cctcactaa gaagacccaa acctctgcat aatgggattt gggctttggg 936

acaagaactg tgacccccaa cctgataaa agagatggaa ggaaaaaaaa aaaaaaa 993

<210> 6
<211> 188
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<213> Nuc. Seq. of SOM175 Absent Exon 6

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1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln

20	25	30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln		
35	40	45
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val		
50	55	60
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly		
65	70	75 80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln		
85	90	95
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly		
100	105	110
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys		
115	120	125
Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg		
130	135	140
Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg		
145	150	155 160
Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu		
165	170	175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
180 185

<210> 7
 <211> 858
 <212> DNA
 <213> Nuc. Seq. of SOM175 Absent Exons 6&7

<220>
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 <222> (3) .. (431)

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 <213> Nuc. Seq. of SOM175 Absent Exons 6&7

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 20 25 30
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
 130 135 140

<210> 9
 <211> 910
 <212> DNA
 <213> Nuc. Seq. of SOM175 Absent Exon 4

<220>
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 <222> (3)..(305)

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 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
 1 5 10 15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 50 55 60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 65 70 75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80 85 90 95

caa gtc cgg atg cag acc taaaaaaaaag gacagtgtg tgaagccaga 335
 Gln Val Arg Met Gln Thr
 100

cagggctgcc actccccacc accgtcccca gccccgttct gttccgggct gggactctgc 395

ccccggagca cccctccccag ctgacatcac ccatccact ccagccccag gccctctgc 455

ccacgtgca cccagcacca ccagcgcct gacccccgga cctgccgtg ccgctgccga 515

cgcgcagct tcctccgttg ccaagggcgg ggcttagagc tcaaccaga cacctgcagg 575

tgccggaagc tgcgaagggtg acacatggct tttcagactc agcaggggtga cttgcctcag 635

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cctcagccca ggcagaagct gctctaggac ctgggcctct cagagggctc ttctgccatc 755

ccttgtctcc ctgaggccat catcaaacag gacagagttg gaagaggaga ctgggaggca 815

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tctgtgcaag taagcatctt acaactggct cttcc 910

<210> 10
 <211> 101
 <212> PRT

<213> Nuc. Seq. of SOM175 Absent Exon 4

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Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Thr
100

<210> 11

<211> 42

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<213> Oligonucleotide

<400> 11

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42

<210> 12

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<212> DNA

<213> Oligonucleotide

<400> 12

agttgtttga ccacattgcc catgagttcc atgctcagag gc

42

<210> 13

<211> 38

<212> DNA

<213> Oligonucleotide

<400> 13

gacccctgggg ctggagtggg atggatgatg tcagctgg

38

<210> 14

<211> 40

<212> DNA

<213> Oligonucleotide

<400> 14

gcgggcagag gacccctgggg ctgtctggcc tcacagcact

40

<210> 15

<211> 236

<212> DNA

<213> Human SOM175

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cccatggtgt atgcaggtcc gagatgctga atacagatcc tcatgcaggt gtcaggcaac 120

ttttcaagac ctaaagacag gtgagctttt ctctccgta ggctgcctcc agccccaggg 180

ccccactcc agccccagac ccagacacct gtagccctgc tcaggtgccg aggtga 236

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<221> CDS

<222> (166)..(831)

<400> 16

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gggggcccgc gaggagccgc cccctgcgcc ccgccccggg tccccgggtc cgcgccatgg 120

ggcggctctg gctgaccccc cccacaccg ccgggctagg gcccg atg agc ccc ctg 177

Met Ser Pro Leu

1

ctg cgt cgc ctg ctg ctt gtt gca ctg ctg cag ctg gct cgc acc cag 225

Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu Ala Arg Thr Gln

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gcc cct gtg tcc cag ttt gat ggc ccc agt cac cag aag aaa gtg gtg	273			
Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln Lys Lys Val Val				
25	30	35		
cca tgg ata gac gtt tat gca cgt gcc aca tgc cag ccc agg gag gtg	321			
Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln Pro Arg Glu Val				
40	45	50		
gtg gtg cct ctg agc atg gaa ctc atg ggc aat gtg gtc aaa caa cta	369			
Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val Val Lys Gln Leu				
55	60	65		
gtg ccc agc tgt gtg act gtg cag cgc tgt ggt ggc tgc tgc cct gac	417			
Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys Cys Pro Asp				
70	75	80		
gat ggc ctg gaa tgt gtg ccc act ggg caa cac caa gtc cga atg cag	465			
Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val Arg Met Gln				
85	90	95	100	
atc ctc atg atc cag tac ccg agc agt cag ctg ggg gag atg tcc ctg	513			
Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly Glu Met Ser Leu				
105	110	115		
gga gaa cac agc caa tgt gaa tgc aga cct aaa aaa aag gag agt gct	561			
Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys Glu Ser Ala				
120	125	130		
gtg agg cca gac agg gtt gcc ata ccc cac cac cgt ccc cag ccc cgc	609			
Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg				
135	140	145		
tct gtt ccg ggc tgg gac tct acc ccg gga gca ccc tcc cca gct gac	657			
Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp				
150	155	160		
atc atc cat ccc act cca gcc cca gga tcc tct gcc cgc ctt gca ccc	705			
Ile Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro				
165	170	175	180	
agc gcc gcc aac gcc ctg acc ccc gga cct gcc gtt gcc gct gta gac	753			
Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp				
185	190	195		
gcc gcc gct tcc tcc att gcc aag ggc ggg gct tag agc tca acc cag	801			
Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala Ser Ser Thr Gln				

a3
cont.

200

205

210

aca cct gta ggt gcc gga agc cgc gaa agt gacaagctgc tttccagact 851
 Thr Pro Val Gly Ala Gly Ser Arg Glu Ser
 215 220

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 aacctcctca gtctgggagg tcaactgcccc aggacctgga ccttttagag agctctctcg 971
 ccatctttta tctcccagag ctgccatcta acaattgtca aggaacctca tgtctcacct 1031
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1242

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 <211> 207
 <212> PRT
 <213> mVRF

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Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
 20 25 30

Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
 35 40 45

Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
 50 55 60

Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95

Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
 100 105 110

Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125

Lys Glu Ser Ala Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg
130 135 140

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro
145 150 155 160

Ser Pro Ala Asp Ile Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala
165 170 175

Arg Leu Ala Pro Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val
180 185 190

Ala Ala Val Asp Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala
195 200 205

<210> 18
<211> 14
<212> PRT
<213> mVRF

<400> 18
Ser Ser Thr Gln Thr Pro Val Gly Ala Gly Ser Arg Glu Ser
1 5 10

<210> 19
<211> 188
<212> PRT
<213> mVRF167

<400> 19
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu
1 5 10 15

Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
20 25 30

Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
50 55 60

Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly

65		70		75		80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln						
	85		90		95	
Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly						
	100		105		110	
Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys						
	115		120		125	
Lys Glu Ser Ala Val Arg Pro Asp Ser Pro Arg Ile Leu Cys Pro Pro						
	130		135		140	
Cys Thr Gln Arg Arg Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg						
	145		150		155	160
Cys Arg Arg Arg Arg Phe Leu His Cys Gln Gly Arg Gly Leu Glu Leu						
	165		170		175	
Asn Pro Asp Thr Cys Arg Cys Arg Lys Pro Arg Lys						
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<400> 20

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	20						25						30						
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln																			
	35						40						45						
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val																			
	50						55						60						
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly																			
	65						70					75						80	
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln																			
	85											90						95	

A3
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Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
130 135 140

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145 150 155 160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
165 170 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
180 185

<210> 21
<211> 71
<212> PRT
<213> mVRF186

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Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly
1 5 10 15

Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp Ile Ile His Pro
20 25 30

Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro Ser Ala Ala Asn
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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly
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Glu Gln Lys Ser His Glu Val Ile Lys Phe Met Asp Val Tyr Gln Arg
35 40 45

Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
50 55 60

Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
65 70 75 80

Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr
85 90 95

Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
100 105 110

Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys Glu
115 120 125

Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Lys Lys Ser Val Arg
130 135 140

Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Phe Lys
145 150 155 160

Ser Trp Ser Val His Cys Glu Pro Cys Ser Glu Arg Arg Lys His Leu
165 170 175

Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp
180 185 190

Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg
195 200 205

Cys Asp Lys Pro Arg Arg
210
